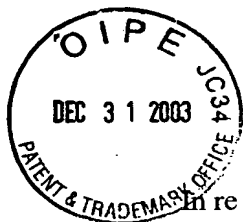


#26
Q 6.1804



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Docket No: Q61014

Yoji IKAWA, et al.

Appln. No.: 09/670,568

Group Art Unit: 1642

Confirmation No.: 5597

Examiner: Yu, M.

Filed: September 27, 2000

For: HUMAN p51 GENES AND GENE PRODUCTS THEREOF

**STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE WITH
37 C.F.R. §§ 1.821-1.825**

MAIL STOP SEQUENCE

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In connection with the Substitute Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. §1.821(g), does not include any new matter;
2. the content of the 30-page Sequence Listing being filed herewith, and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821(c) and (e), respectively, are identical; and
3. all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Applicants respectfully request entry of the Sequence Listing into the application.

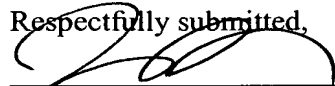
SUGHRUE MION, PLLC
Telephone: (202) 293-7060
Facsimile: (202) 293-7860

WASHINGTON OFFICE

23373

CUSTOMER NUMBER

Respectfully submitted,


Drew Hissong
Registration No. 44,765

Date: December 31, 2003



SEQUENCE LISTING

<110> IKAWA, Yoji
IKAWA, Shuntaro
OBINATA, Masuo

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Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro		
				270					275					280			
att	tta	atc	att	gtt	act	ctg	gaa	acc	aga	gat	ggg	caa	gtc	ctg	ggc	1035	

Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly		
			285					290					295				
cga	cgc	tgc	ttt	gag	gcc	cgg	atc	tgt	gct	tgc	cca	gga	aga	gac	agg	1083	
Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg		
		300					305					310					
aag	gcg	gat	gaa	gat	agc	atc	aga	aag	cag	caa	gtt	tcg	gac	agt	aca	1131	
Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr		
	315					320					325						
aag	aac	ggt	gat	ggt	acg	aag	cgc	ccg	ttt	cgt	cag	aac	aca	cat	ggt	1179	
Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly		
330					335					340					345		
atc	cag	atg	aca	tcc	atc	aag	aaa	cga	aga	tcc	cca	gat	gat	gaa	ctg	1227	
Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu		
				350					355					360			
tta	tac	tta	cca	gtg	agg	ggc	cgt	gag	act	tat	gaa	atg	ctg	ttg	aag	1275	
Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys		
			365					370					375				
atc	aaa	gag	tcc	ctg	gaa	ctc	atg	cag	tac	ctt	cct	cag	cac	aca	att	1323	
Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile		
		380					385					390					
gaa	acg	tac	agg	caa	cag	caa	cag	cag	cag	cac	cag	cac	tta	ctt	cag	1371	
Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln		
	395					400					405						
aaa	cag	acc	tca	ata	cag	tct	cca	tct	tca	tat	ggt	aac	agc	tcc	cca	1419	
Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro		
410					415					420					425		
cct	ctg	aac	aaa	atg	aac	agc	atg	aac	aag	ctg	cct	tct	gtg	agc	cag	1467	
Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val	Ser	Gln		
				430					435					440			
ctt	atc	aac	cct	cag	cag	cgc	aac	gcc	ctc	act	cct	aca	acc	att	cct	1515	
Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr	Ile	Pro		
			445					450						455			
gat	ggc	atg	gga	gcc	aac	att	ccc	atg	atg	ggc	acc	cac	atg	cca	atg	1563	
Asp	Gly	Met	Gly	Ala	Asn	Ile	Pro	Met	Met	Gly	Thr	His	Met	Pro	Met		
		460					465					470					
gct	gga	gac	atg	aat	gga	ctc	agc	ccc	acc	cag	gca	ctc	cct	ccc	cca	1611	
Ala	Gly	Asp	Met	Asn	Gly	Leu	Ser	Pro	Thr	Gln	Ala	Leu	Pro	Pro	Pro		
	475					480					485						
ctc	tcc	atg	cca	tcc	acc	tcc	cac	tgc	aca	ccc	cca	cct	ccg	tat	ccc	1659	
Leu	Ser	Met	Pro	Ser	Thr	Ser	His	Cys	Thr	Pro	Pro	Pro	Pro	Tyr	Pro		
490					495					500					505		
aca	gat	tgc	agc	att	gtc	agt	ttc	tta	gcg	agg	ttg	ggc	tgt	tca	tca	1707	
Thr	Asp	Cys	Ser	Ile	Val	Ser	Phe	Leu	Ala	Arg	Leu	Gly	Cys	Ser	Ser		
				510					515					520			
tgt	ctg	gac	tat	ttc	acg	acc	cag	ggg	ctg	acc	acc	atc	tat	cag	att	1755	

Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile
 525 530 535
 gag cat tac tcc atg gat gat ctg gca agt ctg aaa atc cct gag caa 1803
 Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln
 540 545 550
 ttt cga cat gcg atc tgg aag ggc atc ctg gac cac cgg cag ctc cac 1851
 Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His
 555 560 565
 gaa ttc tcc tcc cct tct cat ctc ctg cgg acc cca agc agt gcc tct 1899
 Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser
 570 575 580 585
 aca gtc agt gtg ggc tcc agt gag acc cgg ggt gag cgt gtt att gat 1947
 Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp
 590 595 600
 gct gtg cga ttc acc ctc cgc cag acc atc tct ttc cca ccc cga gat 1995
 Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp
 605 610 615
 gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat aag caa 2043
 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln
 620 625 630
 cag cgc atc aaa gag gag ggg gag tgagcctcac catgtgagct cttcctatcc 2097
 Gln Arg Ile Lys Glu Glu Gly Glu
 635 640
 ctctcctaac tgccagcccc ctaaaagcac tcttgcttaa tcttcaaagc cttctcccta 2157
 gctcctcccc ttctctttgt ctgattttctt aggggaagga gaagtaagag gctacctctt 2217
 acctaacatc tgacctggca tctaattctg attctggctt taagccttca aaa 2270

<210> 6
 <211> 499
 <212> PRT
 <213> Homo sapien

<400> 6

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
 1 5 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
 20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
 50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
145 150 155 160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg
165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
195 200 205

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
210 215 220

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
225 230 235 240

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
245 250 255

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
260 265 270

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
275 280 285

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
290 295 300

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
305 310 315 320

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
325 330 335

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
340 345 350

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
355 360 365

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
370 375 380

Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser
385 390 395 400

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
405 410 415

Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420 425 430

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
435 440 445

Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
450 455 460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
465 470 475 480

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr
485 490 495

Trp Gly Pro

<210> 7
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus of p51a, p53 and p73 beta

<400> 7

Met Gln Ser Thr Thr Pro Phe Gln His Trp Ser Leu Glu Pro Asp Leu
1 5 10 15

Pro Asn Asn Ser Met Asp Leu Asp Gln Leu Leu Ser Gln Arg Ser Ala
20 25 30

Ser Pro Tyr His Ala Ser Val Pro Thr Pro Ser Pro Tyr Ala Gln Pro
35 40 45

Ser Ser Thr Phe Asp Leu Ser Pro Ser Pro Ile Pro Ser Asn Thr Asp
50 55 60

Tyr Pro Gly Pro His Phe Val Phe Gln Gln Ser Ser Thr Ala Lys Ser
65 70 75 80

Ala Thr Trp Thr Tyr Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala
85 90 95

Lys Thr Cys Pro Ile Gln Ile Lys Val Thr Pro Pro Pro Pro Gly Thr
100 105 110

Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val
115 120 125

Val Lys Arg Cys Pro Asn His Glu Leu Arg Asp Phe Asn Glu Gly Gln
130 135 140

Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Gln Tyr Val Asp
145 150 155 160

Asp Pro Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln
165 170 175

Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser
180 185 190

Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr
195 200 205

Leu Glu Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Arg Ile
210 215 220

Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Arg Lys Gln

225 230 235 240

Gln Ser Lys Asn Gly Thr Lys Arg Ala Phe Gln Asn Thr Lys Lys Arg
245 250 255

Arg Asp Glu Tyr Leu Gln Val Arg Gly Arg Glu Phe Glu Met Leu Lys
260 265 270

Leu Lys Glu Ser Leu Glu Leu Met Pro Gln Tyr Arg Gln Gln Gln Gln
275 280 285

His Leu Lys His Asn Gln Leu Val Pro Arg His Thr Pro Lys Leu Val
290 295 300

Met Phe His Pro Pro Asn Ser Tyr
305 310

<210> 8
<211> 636
<212> PRT
<213> Homo sapien

<400> 8

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 5 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
145 150 155 160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg
165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
195 200 205

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
210 215 220

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
225 230 235 240

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
245 250 255

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
260 265 270

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
275 280 285

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
290 295 300

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
305 310 315 320

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
325 330 335

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
340 345 350

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
355 360 365

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
370 375 380

Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser
385 390 395 400

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
405 410 415

Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420 425 430

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
435 440 445

Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
450 455 460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
465 470 475 480

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe
485 490 495

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln
500 505 510

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu
515 520 525

Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly
530 535 540

Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu
545 550 555 560

Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
565 570 575

Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
580 585 590

Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu
595 600 605

Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
610 615 620

Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
625 630 635

<210> 9
<211> 349
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus of p51B and p73-alpha

<400> 9

Met Gln Ser Thr Thr Phe His Trp Leu Glu Pro Asp Leu Ser Met Asp
1 5 10 15

Gln Leu Leu Ser Gln Ser Ser Pro Tyr His Ala Ser Val Ser Pro Tyr
20 25 30

Ala Gln Pro Ser Ser Thr Phe Asp Ser Pro Pro Ile Pro Ser Asn Thr
35 40 45

Asp Tyr Pro Gly Pro His Phe Val Phe Gln Gln Ser Ser Thr Ala Lys
50 55 60

Ser Ala Thr Trp Thr Tyr Ser Leu Lys Lys Leu Tyr Cys Gln Ile Ala
65 70 75 80

Lys Thr Cys Pro Ile Gln Ile Lys Val Thr Pro Pro Pro Gly Ile Arg
85 90 95

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Val Val Lys Arg
100 105 110

Cys Pro Asn His Glu Leu Arg Phe Asn Glu Gly Gln Ala Pro Ser His
115 120 125

Leu Ile Arg Val Glu Gly Asn Gln Tyr Val Asp Pro Thr Gly Arg Gln
130 135 140

Ser Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr
145 150 155 160

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
165 170 175

Arg Pro Ile Leu Ile Ile Thr Leu Glu Arg Asp Gly Gln Val Leu Gly
180 185 190

Arg Arg Phe Glu Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
195 200 205

Asp Glu Asp Arg Gln Gln Ser Lys Asn Gly Lys Arg Phe Gln Lys Lys
210 215 220

Arg Arg Asp Tyr Leu Val Arg Gly Arg Glu Glu Leu Lys Lys Glu Ser
225 230 235 240

Leu Glu Leu Met Pro Gln Tyr Arg Gln Gln Gln Gln Gln Pro Ser Tyr
245 250 255

Gly Pro Asn Lys Met Asn Lys Leu Pro Ser Val Gln Leu Thr Gly Met
260 265 270

His Ser Ser Met Ser Ser His Cys Thr Pro Pro Pro Pro Tyr Asp Ser
275 280 285

Val Phe Leu Leu Gly Cys Cys Tyr Phe Thr Gln Gly Leu Ile Tyr Asp
290 295 300

Leu Leu Lys Ile Pro Glu Gln Arg Ile Trp Gly Asp Gln His Ser Leu
305 310 315 320

Leu Arg Ala Gly Ser Glu Arg Val Ala Val Phe Arg Thr Ile Pro Arg
325 330 335

Asp Glu Trp Asp Phe Phe Asp Gln Ile Lys Glu Glu Glu
340 345

<210> 10

<211> 1923

<212> DNA

<213> Mus musculus

<400> 10

atgtcgcaga gcacccagac aagcgagttc ctcagcccag aggtcttcca gcatatctgg 60

gattttctgg aacagcctat atgctcagta cagcccatcg agttgaactt tgtggatgaa 120

ccttccgaaa atggtgcaac aaacaagatt gagattagca tggattgtat ccgcatgcaa 180

gactcagacc tcagtgaccc catgtggcca cagtacacga acctggggct cctgaacagc 240
atggaccagc agattcagaa cggctcctcg tccaccagcc cctacaacac agaccacgca 300
cagaatagcg tgacggcgcc ctgcgcctat gcacagccca gctccacctt tgatgccctc 360
tctccatccc ctgccattcc ctccaacaca gattaccgga gccacacag cttcgatgtg 420
tccttcagc agtcaagcac tgccaagtca gccacctgga cgtattccac cgaactgaag 480
aagctgtact gccagattgc gaagacatgc cccatccaga tcaaggtgat gacccccacc 540
ccacagggcg ctgttatccg tgccatgcct gtctacaaga aagctgagca tgtcaccgag 600
gttgtgaaac gatgccctaa ccatgagctg agccgtgagt tcaatgaggg acagattgcc 660
cctcccagtc atctgattcg agtagaaggg aacagccatg cccagtatgt agaagatcct 720
atcacgggaa ggcagagcgt gctggtcctt tatgagccac cacaggttgg cactgaattc 780
acaacagtcc tgtacaattt catgtgtaac agcagctgcg tcggaggaat gaacagacgt 840
ccaattttta tcacgtttac tctggaaacc agagatgggc aagtcctggg ccgacgggtgc 900
tttgaggccc ggatctgtgc ttgccagga agagaccgga aggagatga agacagcatc 960
agaaagcagc aagtatcgga cagcgcaaag aacggcgatg gtacgaagcg ccctttccgt 1020
cagaatacac acggaatcca gatgacttcc atcaagaaac ggagatcccc agatgatgag 1080
ctgctgtacc taccagtgag aggtcgtgag acgtacgaga tgttgctgaa gatcaaagag 1140
tactggagc tcatgcagta cctccctcag cacacgatcg aaacgtacag gcagcagcag 1200
cagcagcagc accagcacct acttcagaaa cagacctcga tgcagtctca gtcttcatat 1260
ggcaacagtt cccacacct gaacaaaatg aacagcatga acaagctgcc ttccgtgagc 1320
cagcttatca accacagca gcgcaatgcc ctactccca ccacatgcc tgagggcatg 1380
ggagccaaca ttctatgat gggcactcac atgccaatgg ctggagacat gaatggactc 1440
agccctaccc aagctctccc tctccactc tccatgcctt ccacctcca ctgcaccca 1500
ccaccgccct accccacaga ctgcagcatt gtcagtttct tagcaagggtt gggctgctca 1560
tcatgcctgg actatttcac gaccagggg ctgaccacca tctatcagat tgagcattac 1620
tccatggatg atttggaag tctgaagatc cctgaacagt tccgacatgc catctggaag 1680
ggcatcctgg accacaggca gctgcacgac ttctcctcac ctctcatct cctgaggacc 1740
ccaagtgggtg cctctaccgt cagtgtgggc tccagtgaga cccgtgggtga acgtgtgatc 1800
gatgccgtgc gctttacct ccgccagacc atctcttttc cccccgtga cgagtggaat 1860
gatttcaact ttgacatgga ttctcgtcgc aacaagcagc agcgtatcaa agaggaagga 1920
gaa 1923

<210> 11
<211> 641
<212> PRT
<213> Mus musculus

<400> 11

Met Ser Gln Ser Thr Gln Thr Ser Glu Phe Leu Ser Pro Glu Val Phe
1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
20 25 30

Ile Glu Leu Asn Phe Val Asp Glu Pro Ser Glu Asn Gly Ala Thr Asn
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
180 185 190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
195 200 205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
210 215 220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
245 250 255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
260 265 270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
275 280 285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Ala Lys Asn Gly Asp Gly Thr Lys
325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Met Gln Ser
405 410 415

Gln Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
420 425 430

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
435 440 445

Asn Ala Leu Thr Pro Thr Thr Met Pro Glu Gly Met Gly Ala Asn Ile
450 455 460

Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
465 470 475 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
485 490 495

His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
500 505 510

Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
515 520 525

Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
530 535 540

Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
545 550 555 560

Gly Ile Leu Asp His Arg Gln Leu His Asp Phe Ser Ser Pro Pro His
565 570 575

Leu Leu Arg Thr Pro Ser Gly Ala Ser Thr Val Ser Val Gly Ser Ser
580 585 590

Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
595 600 605

Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
610 615 620

Asp Met Asp Ser Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
625 630 635 640

Glu

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> p73-F1 sense primer

<400> 12
tacgtgcacg taaagacacg ttgctcc

27

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> p73-R1 antisense primer

<400> 13
tgctgcacgt tgctccacgt ggacgtacg

29

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> p73-F2 sense primer

<400> 14
tacgtatact acgacgtgta cgtgaaggg

29

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> p73-R2 antisense primer

<400> 15
atgaactacg acgtacgacg tccacgtat

29

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence encoding HA peptide tag

<400> 16
atgtatccat atgatgttcc agattatgct

30

<210> 17
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<212> PRT
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